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SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: STEINMAN, RALPH A  
NUSSENZWEIG, MICHEL C  
SWIGGARD, WILLIAM J  
JIANG, WANPING

(ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH  
C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND  
USES THEREOF

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Klauber & Jackson  
(B) STREET: 411 Hackensack Avenue  
(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/381,528  
(B) FILING DATE: 31-JAN-1995  
(C) CLASSIFICATION:

(vii) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US96/01383  
(B) FILING DATE: 31-JAN-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-081 PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201 487-5800  
(B) TELEFAX: 201 343-1684  
(C) TELEX: 133521

(x) Note: In all the amino acid sequences below, "Xaa" stands for one of  
the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: cytoplasmic domain of human DEC-205

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1			5					10						15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20				25						30			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: human DEC-205, peptide N1

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Glu	Ser	Ser	Gly	Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr
1			5					10					15		
Gly	Lys	Cys	Ile	Gln	Pro	Leu	Phe	Asp							
		20				25									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1723 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: predicted amino acid sequence of DEC-205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Arg	Thr	Gly	Arg	Val	Thr	Pro	Gly	Leu	Ala	Ala	Gly	Leu	Leu	Leu
1			5					10					15		

Leu	Leu	Leu	Arg	Ser	Phe	Gly	Leu	Val	Glu	Pro	Ser	Glu	Ser	Ser	Gly			
			20					25					30					
Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Glu	Asn	Thr	Gly	Lys	Cys	Ile	Gln			
		35					40					45						
Pro	Leu	Ser	Asp	Trp	Val	Val	Ala	Gln	Asp	Cys	Ser	Gly	Thr	Asn	Asn			
		50				55					60							
Met	Leu	Trp	Lys	Trp	Val	Ser	Gln	His	Arg	Leu	Phe	His	Leu	Glu	Ser			
		65			70					75					80			
Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ala	Thr	Asp	Asn	Leu	Arg			
				85					90					95				
Met	Phe	Ser	Cys	Asp	Ser	Thr	Val	Met	Leu	Trp	Trp	Lys	Cys	Glu	His			
			100					105					110					
His	Ser	Leu	Tyr	Thr	Ala	Ala	Gln	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly			
		115					120					125						
Tyr	Ala	Val	Ala	Asn	Thr	Asn	Thr	Ser	Asp	Val	Trp	Lys	Lys	Gly	Gly			
		130				135					140							
Ser	Glu	Glu	Asn	Leu	Cys	Ala	Gln	Pro	Tyr	His	Glu	Ile	Tyr	Thr	Arg			
		145			150					155					160			
Asp	Gly	Asn	Ser	Tyr	Gly	Arg	Pro	Cys	Glu	Phe	Pro	Phe	Leu	Ile	Gly			
				165					170					175				
Glu	Thr	Trp	Tyr	His	Asp	Cys	Ile	His	Asp	Glu	Asp	His	Ser	Gly	Pro			
			180					185					190					
Trp	Cys	Ala	Thr	Thr	Leu	Ser	Tyr	Glu	Tyr	Asp	Gln	Lys	Trp	Gly	Ile			
		195					200					205						
Cys	Leu	Leu	Pro	Glu	Ser	Gly	Cys	Glu	Gly	Asn	Trp	Glu	Lys	Asn	Glu			
		210				215					220							
Gln	Ile	Gly	Ser	Cys	Tyr	Gln	Phe	Asn	Asn	Gln	Glu	Ile	Leu	Ser	Trp			
		225			230					235					240			
Lys	Glu	Ala	Tyr	Val	Ser	Cys	Gln	Asn	Gln	Gly	Ala	Asp	Leu	Leu	Ser			
				245					250					255				
Ile	His	Ser	Ala	Ala	Glu	Leu	Ala	Tyr	Ile	Thr	Gly	Lys	Glu	Asp	Ile			
			260					265					270					
Ala	Arg	Leu	Val	Trp	Leu	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly			
		275					280					285						
Trp	Glu	Trp	Ser	Asp	Phe	Arg	Pro	Leu	Lys	Phe	Leu	Asn	Trp	Asp	Pro			
		290				295					300							
Gly	Thr	Pro	Val	Ala	Pro	Val	Ile	Gly	Gly	Ser	Ser	Cys	Ala	Arg	Met			
		305			310					315					320			
Asp	Thr	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Val	Ser	Cys	Glu	Ser	Gln	Gln			
				325				330						335				

Pro Tyr Val Cys Lys Lys Pro Leu Asn Asn Thr Leu Glu Leu Pro Asp  
 340 345 350  
 Val Trp Thr Tyr Thr Asp Thr His Cys His Val Gly Trp Leu Pro Asn  
 355 360 365  
 Asn Gly Phe Cys Tyr Leu Leu Ala Asn Glu Ser Ser Ser Trp Asp Ala  
 370 375 380  
 Ala His Leu Lys Cys Lys Ala Phe Gly Ala Asp Leu Ile Ser Met His  
 385 390 395 400  
 Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Gly Asp  
 405 410 415  
 Val Lys Lys Glu Ile Trp Thr Gly Leu Lys Asn Thr Asn Ser Pro Ala  
 420 425 430  
 Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asn  
 435 440 445  
 Glu Asn Glu Pro Ser Val Pro Phe Asn Lys Thr Pro Asn Cys Val Ser  
 450 455 460  
 Tyr Leu Gly Lys Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Lys Lys  
 465 470 475 480  
 Leu Arg Tyr Val Cys Lys Lys Lys Gly Glu Ile Thr Lys Asp Ala Glu  
 485 490 495  
 Ser Asp Lys Leu Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu  
 500 505 510  
 Thr Cys Tyr Lys Ile Tyr Glu Lys Glu Ala Pro Phe Gly Thr Asn Cys  
 515 520 525  
 Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Phe Leu Asn Tyr Met  
 530 535 540  
 Met Lys Asn Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu  
 545 550 555 560  
 Arg Asp Pro Asp Ser Arg Gly Glu Tyr Ser Trp Ala Val Ala Gln Gly  
 565 570 575  
 Val Lys Gln Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala  
 580 585 590  
 Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Thr Leu Gly Lys  
 595 600 605  
 Trp Glu Val Lys Asn Cys Arg Ser Phe Arg Ala Leu Ser Ile Cys Lys  
 610 615 620  
 Lys Val Ser Glu Pro Gln Glu Pro Glu Glu Ala Ala Pro Lys Pro Asp  
 625 630 635 640  
 Asp Pro Cys Pro Glu Gly Trp His Thr Phe Pro Ser Ser Leu Ser Cys  
 645 650 655

Tyr	Lys	Val	Phe	His	Ile	Glu	Arg	Ile	Val	Arg	Lys	Arg	Asn	Trp	Glu
			660						665			670			
Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Pro	Ser	Phe
			675						680			685			
Ser	Arg	Arg	Glu	Glu	Ile	Lys	Asp	Phe	Val	His	Leu	Leu	Lys	Asp	Gln
			690						695			700			
Phe	Ser	Gly	Gln	Arg	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro
			705						710			715			
Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Ala
			725						730			735			
Val	Met	Met	Glu	Pro	Glu	Phe	Gln	Gln	Asp	Phe	Asp	Ile	Arg	Asp	Cys
			740						745			750			
Ala	Ala	Ile	Lys	Val	Leu	Asp	Val	Pro	Trp	Arg	Arg	Val	Trp	His	Leu
			755						760			765			
Tyr	Glu	Asp	Lys	Asp	Tyr	Ala	Tyr	Trp	Lys	Pro	Phe	Ala	Cys	Asp	Ala
			770						775			780			
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Ser	Thr	Pro	Gln	Met
			785						790			795			
Pro	Asp	Trp	Tyr	Asn	Pro	Glu	Arg	Thr	Gly	Ile	His	Gly	Pro	Pro	Val
			805						810			815			
Ile	Ile	Glu	Gly	Ser	Glu	Tyr	Trp	Phe	Val	Ala	Asp	Pro	His	Leu	Asn
			820						825			830			
Tyr	Glu	Glu	Ala	Val	Leu	Tyr	Cys	Ala	Ser	Asn	His	Ser	Phe	Leu	Ala
			835						840			845			
Thr	Ile	Thr	Ser	Phe	Thr	Gly	Leu	Lys	Ala	Ile	Lys	Asn	Lys	Leu	Ala
			850						855			860			
Asn	Ile	Ser	Gly	Glu	Glu	Gln	Lys	Trp	Trp	Val	Lys	Thr	Ser	Glu	Asn
			865						870			875			
Pro	Ile	Asp	Arg	Tyr	Phe	Leu	Gly	Ser	Arg	Arg	Arg	Leu	Trp	His	His
			885						890			895			
Phe	Pro	Met	Thr	Phe	Gly	Asp	Glu	Cys	Leu	His	Met	Ser	Ala	Lys	Thr
			900						905			910			
Trp	Leu	Val	Asp	Leu	Ser	Lys	Arg	Ala	Asp	Cys	Asn	Ala	Lys	Leu	Pro
			915						920			925			
Phe	Ile	Cys	Glu	Arg	Tyr	Asn	Val	Ser	Ser	Leu	Glu	Lys	Tyr	Ser	Pro
			930						935			940			
Asp	Pro	Ala	Ala	Lys	Val	Gln	Cys	Thr	Glu	Lys	Trp	Ile	Pro	Phe	Gln
			945						950			955			
Asn	Lys	Cys	Phe	Leu	Lys	Val	Asn	Ser	Gly	Pro	Val	Thr	Phe	Ser	Gln
			965						970			975			

Ala Ser Gly	Ile Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu
980	985 990
Ser Arg Gly	Glu Gln Asp Phe Ile Ile Ser Leu Leu Pro Glu Met Glu
995	1000 1005
Ala Ser Leu Trp	Ile Gly Leu Arg Trp Thr Ala Tyr Glu Arg Ile Asn
1010	1015 1020
Arg Trp Thr Asp	Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro Leu
1025	1030 1035 1040
Leu Val Gly Arg	Arg Leu Ser Ile Pro Thr Asn Phe Phe Asp Asp Glu
	1045 1050 1055
Ser His Phe His	Cys Ala Leu Ile Leu Asn Leu Lys Lys Ser Pro Leu
	1060 1065 1070
Thr Gly Thr Trp	Asn Phe Thr Ser Cys Ser Glu Arg His Ser Leu Ser
	1075 1080 1085
Leu Cys Gln Lys	Tyr Ser Glu Thr Glu Asp Gly Gln Pro Trp Glu Asn
	1090 1095 1100
Thr Ser Lys Thr	Val Lys Tyr Leu Asn Asn Leu Tyr Lys Ile Ile Ser
1105	1110 1115 1120
Lys Pro Leu Thr	Trp His Gly Ala Leu Lys Glu Cys Met Lys Glu Lys
	1125 1130 1135
Met Arg Leu Val	Ser Ile Thr Asp Pro Tyr Gln Gln Ala Phe Leu Ala
	1140 1145 1150
Val Gln Ala Thr	Leu Arg Asn Ser Ser Phe Trp Ile Gly Leu Ser Ser
	1155 1160 1165
Gln Asp Asp Glu	Leu Asn Phe Gly Trp Ser Asp Gly Lys Arg Leu Gln
	1170 1175 1180
Phe Ser Asn Trp	Ala Gly Ser Asn Glu Gln Leu Asp Asp Cys Val Ile
1185	1190 1195 1200
Leu Asp Thr Asp	Gly Phe Trp Lys Thr Ala Asp Cys Asp Asp Asn Gln
	1205 1210 1215
Pro Gly Ala Ile	Cys Tyr Tyr Pro Gly Asn Glu Thr Glu Glu Glu Val
	1220 1225 1230
Arg Ala Leu Asp	Thr Ala Lys Cys Pro Ser Pro Val Gln Ser Thr Pro
	1235 1240 1245
Trp Ile Pro Phe	Gln Asn Ser Cys Tyr Asn Phe Met Ile Thr Asn Asn
	1250 1255 1260
Arg His Lys Thr	Val Thr Pro Glu Glu Val Gln Ser Thr Cys Glu Lys
1265	1270 1275 1280
Leu His Pro Lys	Ala His Ser Leu Ser Ile Arg Asn Glu Glu Glu Asn
	1285 1290 1295

Thr Phe Val Val Glu Gln Leu Leu Tyr Phe Asn Tyr Ile Ala Ser Trp	1300	1305	1310
Val Met Leu Gly Ile Thr Tyr Glu Asn Asn Ser Leu Met Trp Phe Asp	1315	1320	1325
Lys Thr Ala Leu Ser Tyr Thr His Trp Arg Thr Gly Arg Pro Thr Val	1330	1335	1340
Lys Asn Gly Lys Phe Leu Ala Gly Leu Ser Thr Asp Gly Phe Trp Asp	1345	1350	1355
Ile Gln Ser Phe Asn Val Ile Glu Glu Thr Leu His Phe Tyr Gln His	1365	1370	1375
Ser Ile Ser Ala Cys Lys Ile Glu Met Val Asp Tyr Glu Asp Lys His	1380	1385	1390
Asn Gly Thr Leu Pro Gln Phe Ile Pro Tyr Lys Asp Gly Val Tyr Ser	1395	1400	1405
Val Ile Gln Lys Lys Val Thr Trp Tyr Glu Ala Leu Asn Ala Cys Ser	1410	1415	1420
Gln Ser Gly Gly Glu Leu Ala Ser Val His Asn Pro Asn Gly Lys Leu	1425	1430	1435
Phe Leu Glu Asp Ile Val Asn Arg Asp Gly Phe Pro Leu Trp Val Gly	1445	1450	1455
Leu Ser Ser His Asp Gly Ser Glu Ser Ser Phe Glu Trp Ser Asp Gly	1460	1465	1470
Arg Ala Phe Asp Tyr Val Pro Trp Gln Ser Leu Gln Ser Pro Gly Asp	1475	1480	1485
Cys Val Val Leu Tyr Pro Lys Gly Ile Trp Arg Arg Glu Lys Cys Leu	1490	1495	1500
Ser Val Lys Asp Gly Ala Ile Cys Tyr Lys Pro Thr Lys Asp Lys Lys	1505	1510	1515
Leu Ile Phe His Val Lys Ser Ser Lys Cys Pro Val Ala Lys Arg Asp	1525	1530	1535
Gly Pro Gln Trp Val Gln Tyr Gly Gly His Cys Tyr Ala Ser Asp Gln	1540	1545	1550
Val Leu His Ser Phe Ser Glu Ala Lys Gln Val Cys Gln Glu Leu Asp	1555	1560	1565
His Ser Ala Thr Val Val Thr Ile Ala Asp Glu Asn Glu Asn Lys Phe	1570	1575	1580
Val Ser Arg Leu Met Arg Glu Asn Tyr Asn Ile Thr Met Arg Val Trp	1585	1590	1595
Leu Gly Leu Ser Gln His Ser Leu Asp Gln Ser Trp Ser Trp Leu Asp	1605	1610	1615

Gly Leu Asp Val Thr Phe Val Lys Trp Glu Asn Lys Thr Lys Asp Gly  
 1620 1625 1630  
 Asp Gly Lys Cys Ser Ile Leu Ile Ala Ser Asn Glu Thr Trp Arg Lys  
 1635 1640 1645  
 Val His Cys Ser Arg Gly Tyr Ala Arg Ala Val Cys Lys Ile Pro Leu  
 1650 1655 1660  
 Ser Pro Asp Tyr Thr Gly Ile Ala Ile Leu Phe Ala Val Leu Cys Leu  
 1665 1670 1675 1680  
 Leu Gly Leu Ile Ser Leu Ala Ile Trp Phe Leu Leu Gln Arg Ser His  
 1685 1690 1695  
 Ile Arg Trp Thr Gly Phe Ser Ser Val Arg Tyr Glu His Gly Thr Asn  
 1700 1705 1710  
 Glu Asp Glu Val Met Leu Pro Ser Phe His Asp  
 1715 1720

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: bovine PLA2 receptor

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: bovine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Leu Leu Ser Leu Ser Leu Leu Leu Leu Leu Gln Val Pro  
 1 5 10 15  
 Ala Gly Ser Ala Glu Thr Ala Ala Trp Ala Val Thr Pro Glu Arg Leu  
 20 25 30  
 Arg Glu Trp Gln Asp Lys Gly Ile Phe Ile Ile Gln Ser Glu Asn Leu  
 35 40 45  
 Glu Lys Cys Ile Gln Ala Ser Lys Ser Thr Leu Thr Leu Glu Asn Cys  
 50 55 60  
 Lys Pro Pro Asn Lys Tyr Met Leu Trp Lys Trp Val Ser Asn His Arg  
 65 70 75 80  
 Leu Phe Asn Ile Gly Gly Ser Gly Cys Leu Gly Leu Asn Val Ser Ser  
 85 90 95  
 Pro Glu Gln Pro Leu Ser Ile Tyr Glu Cys Asp Ser Thr His Val Ser



100					105					110					
Leu	Lys	Trp	His	Cys	Asn	Lys	Lys	Thr	Ile	Thr	Gly	Pro	Leu	Gln	Tyr
115					120					125					
Leu	Val	Gln	Val	Lys	Gln	Asp	Asn	Thr	Leu	Val	Ala	Ser	Arg	Lys	Tyr
130					135					140					
Leu	His	Lys	Trp	Val	Ser	Tyr	Met	Ser	Gly	Gly	Gly	Gly	Ile	Cys	Asp
145					150					155					
Tyr	Leu	His	Lys	Asp	Leu	Tyr	Thr	Ile	Lys	Gly	Asn	Ala	His	Gly	Thr
165					170					175					
Pro	Cys	Met	Phe	Pro	Phe	Gln	Tyr	Asn	Gln	Gln	Trp	His	His	Glu	Cys
180					185					190					
Thr	Arg	Glu	Gly	Arg	Glu	Asp	Asn	Leu	Leu	Trp	Cys	Ala	Thr	Thr	Ser
195					200					205					
Arg	Tyr	Glu	Arg	Asp	Glu	Lys	Trp	Gly	Phe	Cys	Pro	Asp	Pro	Thr	Ser
210					215					220					
Thr	Glu	Val	Gly	Cys	Asp	Ala	Val	Trp	Glu	Lys	Asp	Leu	His	Ser	Arg
225					230					235					
Ile	Cys	Tyr	Gln	Phe	Asn	Leu	Leu	Ser	Ser	Leu	Ser	Trp	Ser	Glu	Ala
245					250					255					
His	Ser	Ser	Cys	Gln	Met	Gln	Gly	Ala	Ala	Leu	Leu	Ser	Ile	Ala	Asp
260					265					270					
Glu	Thr	Glu	Glu	Asn	Phe	Val	Arg	Lys	His	Leu	Gly	Ser	Glu	Ala	Val
275					280					285					
Glu	Val	Trp	Met	Gly	Leu	Asn	Gln	Leu	Asp	Glu	Asp	Ala	Gly	Trp	Gln
290					295					300					
Trp	Ser	Asp	Arg	Thr	Pro	Leu	Asn	Tyr	Leu	Asn	Trp	Lys	Pro	Glu	Ile
305					310					315					
Asn	Phe	Glu	Pro	Phe	Val	Glu	Tyr	His	Cys	Gly	Thr	Phe	Asn	Ala	Phe
325					330					335					
Met	Pro	Lys	Ala	Trp	Lys	Ser	Arg	Asp	Cys	Glu	Ser	Thr	Leu	Pro	Tyr
340					345					350					
Val	Cys	Lys	Lys	Tyr	Leu	Asn	Pro	Thr	Asp	His	Gly	Val	Val	Glu	Lys
355					360					365					
Asp	Ala	Trp	Lys	Tyr	Tyr	Ala	Thr	His	Cys	Glu	Pro	Gly	Trp	Asn	Pro
370					375					380					
His	Asn	Arg	Asn	Cys	Tyr	Lys	Leu	Gln	Lys	Glu	Lys	Lys	Thr	Trp	Asn
385					390					395					
Glu	Ala	Leu	Gln	Ser	Cys	Gln	Ser	Asn	Asn	Ser	Val	Leu	Thr	Asp	Ile
405					410					415					
Thr	Ser	Leu	Ala	Glu	Val	Glu	Phe	Leu	Val	Thr	Leu	Leu	Gly	Asp	Glu

420					425					430						
Asn	Ala	Ser	Glu	Thr	Trp	Ile	Gly	Leu	Ser	Ser	His	Lys	Ile	Pro	Val	
435					440					445						
Ser	Phe	Glu	Trp	Ser	Asn	Gly	Ser	Ser	Val	Thr	Phe	Thr	Asn	Trp	His	
450					455					460						
Thr	Leu	Glu	Pro	His	Ile	Phe	Pro	Asn	Arg	Ser	Gln	Leu	Cys	Val	Ser	
465					470					475					480	
Ala	Glu	Gln	Ser	Glu	Gly	His	Trp	Lys	Val	Lys	Asn	Cys	Glu	Glu	Thr	
485					490					495						
Leu	Phe	Tyr	Leu	Cys	Lys	Lys	Thr	His	Leu	Val	Leu	Ser	Asp	Thr	Glu	
500					505					510						
Ser	Gly	Cys	Gln	Lys	Gly	Trp	Glu	Arg	His	Gly	Lys	Phe	Cys	Tyr	Lys	
515					520					525						
Ile	Asp	Thr	Val	Leu	Arg	Ser	Phe	Asp	His	Ala	Ser	Ser	Gly	Tyr	Tyr	
530					535					540						
Cys	Pro	Pro	Ala	Leu	Ile	Thr	Ile	Thr	Ser	Arg	Phe	Glu	Gln	Ala	Phe	
545					550					555					560	
Ile	Thr	Ser	Leu	Ile	Ser	Ser	Val	Val	Lys	Thr	Lys	Asp	Thr	Tyr	Phe	
565					570					575						
Trp	Ile	Ala	Leu	Gln	Asp	Gln	Asn	Asn	Thr	Gly	Glu	Tyr	Thr	Trp	Lys	
580					585					590						
Thr	Ala	Gly	Gln	Gln	Leu	Glu	Pro	Val	Lys	Tyr	Thr	His	Trp	Asn	Thr	
595					600					605						
Arg	Gln	Pro	Arg	Tyr	Ser	Gly	Gly	Cys	Val	Val	Met	Arg	Gly	Arg	Ser	
610					615					620						
His	Pro	Gly	Arg	Trp	Glu	Val	Arg	Asp	Cys	Arg	His	Phe	Lys	Ala	Met	
625					630					635					640	
Ser	Leu	Cys	Lys	Gln	Pro	Val	Glu	Asn	Arg	Glu	Lys	Thr	Lys	Gln	Glu	
645					650					655						
Glu	Gly	Trp	Pro	Phe	His	Pro	Cys	Tyr	Leu	Asp	Trp	Glu	Ser	Glu	Pro	
660					665					670						
Gly	Leu	Ala	Ser	Cys	Phe	Lys	Val	Phe	His	Ser	Glu	Lys	Val	Leu	Met	
675					680					685						
Lys	Arg	Thr	Trp	Arg	Gln	Ala	Glu	Glu	Phe	Cys	Glu	Glu	Phe	Gly	Ala	
690					695					700						
His	Leu	Ala	Ser	Phe	Ala	His	Ile	Glu	Glu	Glu	Asn	Phe	Val	Asn	Glu	
705					710					715					720	
Leu	Leu	His	Ser	Lys	Phe	Asn	Arg	Thr	Glu	Glu	Arg	Gln	Phe	Trp	Ile	
725					730					735						
Gly	Phe	Asn	Lys	Arg	Asn	Pro	Leu	Asn	Ala	Gly	Ser	Trp	Glu	Trp	Ser	

740					745					750					
Asp	Gly	Thr	Pro	Val	Val	Ser	Ser	Phe	Leu	Asp	Asn	Ser	Tyr	Phe	Gly
	755						760					765			
Glu	Asp	Ala	Arg	Asn	Cys	Ala	Val	Tyr	Lys	Ala	Asn	Lys	Thr	Leu	Leu
	770					775					780				
Pro	Ser	Tyr	Cys	Gly	Ser	Lys	Arg	Glu	Trp	Ile	Cys	Lys	Ile	Pro	Arg
	785					790					795				800
Asp	Val	Arg	Pro	Lys	Val	Pro	Pro	Trp	Tyr	Gln	Tyr	Asp	Ala	Pro	Trp
				805					810					815	
Leu	Phe	Tyr	Gln	Asp	Ala	Glu	Tyr	Leu	Phe	His	Ile	Ser	Ala	Ser	Glu
			820					825					830		
Trp	Ser	Ser	Phe	Glu	Phe	Val	Cys	Gly	Trp	Leu	Arg	Ser	Asp	Ile	Leu
		835					840						845		
Thr	Ile	His	Ser	Ala	His	Glu	Gln	Glu	Phe	Ile	His	Ser	Lys	Ile	Arg
	850					855					860				
Ala	Leu	Ser	Lys	Tyr	Gly	Val	Asn	Trp	Trp	Ile	Gly	Leu	Arg	Glu	Glu
	865					870					875				880
Arg	Ala	Ser	Asp	Glu	Phe	Arg	Trp	Arg	Asp	Gly	Ser	Pro	Val	Ile	Tyr
				885					890					895	
Gln	Asn	Trp	Asp	Lys	Gly	Lys	Glu	Arg	Ser	Met	Gly	Leu	Asn	Glu	Ser
			900					905					910		
Gln	Arg	Cys	Gly	Phe	Ile	Ser	Ser	Ile	Thr	Gly	Leu	Trp	Ala	Ser	Glu
		915					920						925		
Glu	Cys	Ser	Ile	Ser	Met	Pro	Ser	Ile	Cys	Lys	Arg	Lys	Lys	Val	Trp
	930					935					940				
Val	Ile	Glu	Lys	Lys	Lys	Asp	Ile	Pro	Lys	Gln	His	Gly	Thr	Cys	Pro
	945					950					955				960
Lys	Gly	Trp	Leu	Tyr	Phe	Asp	Tyr	Lys	Cys	Leu	Leu	Leu	Lys	Ile	Pro
			965						970					975	
Glu	Gly	Pro	Ser	Asp	Trp	Lys	Asn	Trp	Thr	Ser	Ala	Gln	Asp	Phe	Cys
			980					985					990		
Val	Glu	Glu	Gly	Gly	Thr	Leu	Val	Ala	Ile	Glu	Asn	Glu	Val	Glu	Gln
		995					1000					1005			
Ala	Phe	Ile	Thr	Met	Asn	Leu	Phe	Gly	His	Thr	Thr	Asn	Val	Trp	Ile
	1010					1015					1020				
Gly	Leu	Gln	Asp	Asp	Asp	Tyr	Glu	Lys	Trp	Leu	Asn	Gly	Arg	Pro	Val
	1025					1030					1035				1040
Ser	Tyr	Ser	Asn	Trp	Ser	Pro	Phe	Asp	Thr	Lys	Asn	Ile	Pro	Asn	His
			1045						1050					1055	
Asn	Thr	Thr	Glu	Val	Gln	Lys	Arg	Ile	Pro	Leu	Cys	Gly	Leu	Leu	Ser

1060					1065					1070					
Asn	Asn	Pro	Asn	Phe	His	Phe	Thr	Gly	Lys	Trp	Tyr	Phe	Asp	Cys	Arg
1075					1080					1085					
Glu	Gly	Tyr	Gly	Phe	Val	Cys	Glu	Lys	Met	Gln	Asp	Ala	Ser	Gly	His
1090					1095					1100					
Ser	Ile	Asn	Thr	Ser	Asp	Met	Tyr	Pro	Ile	Pro	Asn	Thr	Leu	Glu	Tyr
1105					1110					1115					1120
Gly	Asn	Arg	Thr	Tyr	Lys	Ile	Ile	Asn	Ala	Asn	Met	Thr	Trp	Tyr	Thr
1125					1130					1135					
Ala	Leu	Lys	Thr	Cys	Leu	Met	His	Gly	Ala	Glu	Leu	Ala	Ser	Ile	Thr
1140					1145					1150					
Asp	Gln	Tyr	His	Gln	Ser	Phe	Leu	Thr	Val	Ile	Leu	Asn	Arg	Val	Gly
1155					1160					1165					
Tyr	Ala	His	Trp	Ile	Gly	Leu	Phe	Thr	Glu	Asp	Asn	Gly	Leu	Ser	Phe
1170					1175					1180					
Asp	Trp	Ser	Asp	Gly	Thr	Lys	Ser	Ser	Phe	Thr	Phe	Trp	Lys	Asp	Asp
1185					1190					1195					1200
Glu	Ser	Ser	Phe	Leu	Gly	Asp	Cys	Val	Phe	Ala	Asp	Thr	Ser	Gly	Arg
1205					1210					1215					
Trp	Ser	Ser	Thr	Ala	Cys	Glu	Ser	Tyr	Leu	Gln	Gly	Ala	Ile	Cys	Gln
1220					1225					1230					
Val	Pro	Thr	Glu	Thr	Arg	Leu	Ser	Gly	Arg	Leu	Glu	Leu	Cys	Ser	Glu
1235					1240					1245					
Thr	Ser	Ile	Pro	Trp	Ile	Lys	Phe	Lys	Ser	Asn	Cys	Tyr	Ser	Phe	Ser
1250					1255					1260					
Thr	Val	Leu	Glu	Ser	Thr	Ser	Phe	Glu	Ala	Ala	His	Glu	Phe	Cys	Lys
1265					1270					1275					1280
Lys	Lys	Gly	Ser	Asn	Leu	Leu	Thr	Ile	Lys	Asp	Glu	Ala	Glu	Asn	Ser
1285					1290					1295					
Phe	Leu	Leu	Glu	Glu	Leu	Leu	Ala	Phe	Arg	Ser	Ser	Val	Gln	Met	Ile
1300					1305					1310					
Trp	Leu	Asn	Ala	Gln	Phe	Asp	Gly	Asp	Asn	Glu	Thr	Ile	Lys	Trp	Phe
1315					1320					1325					
Asp	Gly	Thr	Pro	Thr	Asp	Gln	Ser	Asn	Trp	Gly	Ile	Arg	Lys	Pro	Glu
1330					1335					1340					
Val	Tyr	His	Phe	Lys	Pro	His	Leu	Cys	Val	Ala	Leu	Arg	Ile	Pro	Glu
1345					1350					1355					1360
Gly	Val	Trp	Gln	Leu	Ser	Ser	Cys	Gln	Asp	Lys	Lys	Gly	Phe	Ile	Cys
1365					1370					1375					
Lys	Met	Glu	Ala	Asp	Ile	His	Thr	Val	Lys	Lys	His	Pro	Gly	Lys	Gly

1380	1385	1390
Pro Ser His Ser Val Ile Pro Leu Thr Val Ala Leu Thr Leu Leu Val		
1395	1400	1405
Ile Leu Ala Ile Ser Thr Leu Ser Phe Cys Met Tyr Lys His Ser His		
1410	1415	1420
Ile Ile Phe Gly Arg Leu Ala Gln Phe Arg Asn Pro Tyr Tyr Pro Ser		
1425	1430	1435
Ala Asn Phe Ser Thr Val His Leu Glu Glu Asn Ile Leu Ile Ser Asp		
1445	1450	1455
Leu Glu Lys Asn Asp Gln		
1460		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1457 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (A) DESCRIPTION: human macrophage mannose receptor
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: human
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Leu Pro Leu Leu Leu Val Phe Ala Ser Val Ile Pro Gly Ala		
1	5	10
Val Leu Leu Leu Asp Thr Arg Gln Phe Leu Ile Tyr Asn Glu Asp His		
20	25	30
Lys Arg Cys Val Asp Ala Val Ser Pro Ser Ala Val Gln Thr Ala Ala		
35	40	45
Cys Asn Gln Asp Ala Glu Ser Gln Lys Phe Arg Trp Val Ser Glu Ser		
50	55	60
Gln Ile Met Ser Val Ala Phe Lys Leu Cys Leu Gly Val Pro Ser Lys		
65	70	75
Thr Asp Trp Val Ala Ile Thr Leu Tyr Ala Cys Asp Ser Lys Ser Glu		
85	90	95
Phe Gln Lys Trp Glu Cys Lys Asn Asp Thr Leu Leu Gly Ile Lys Gly		
100	105	110
Glu Asp Leu Phe Phe Asn Tyr Gly Asn Arg Gln Glu Lys Asn Ile Met		
115	120	125

Leu Tyr Lys Gly Ser Gly Leu Trp Ser Arg Trp Lys Ile Tyr Gly Thr  
 130 135 140  
 Thr Asp Asn Leu Cys Ser Arg Gly Tyr Glu Ala Met Tyr Thr Leu Leu  
 145 150 155 160  
 Gly Asn Ala Asn Gly Ala Thr Cys Ala Phe Pro Phe Lys Phe Glu Asn  
 165 170 175  
 Lys Trp Tyr Ala Asp Cys Thr Ser Ala Gly Arg Ser Asp Gly Trp Leu  
 180 185 190  
 Trp Cys Gly Thr Thr Thr Asp Tyr Asp Thr Asp Lys Leu Phe Gly Tyr  
 195 200 205  
 Cys Pro Leu Lys Phe Glu Gly Ser Glu Ser Leu Trp Asn Lys Asp Pro  
 210 215 220  
 Leu Thr Ser Val Ser Tyr Gln Ile Asn Ser Lys Ser Ala Leu Thr Trp  
 225 230 235 240  
 His Gln Ala Arg Lys Ser Cys Gln Gln Gln Asn Ala Glu Leu Leu Ser  
 245 250 255  
 Ile Thr Glu Ile His Glu Gln Thr Tyr Leu Thr Gly Leu Thr Ser Ser  
 260 265 270  
 Leu Thr Ser Gly Leu Trp Ile Gly Leu Asn Ser Leu Ser Phe Asn Ser  
 275 280 285  
 Gly Trp Gln Trp Ser Asp Arg Ser Pro Phe Arg Tyr Leu Asn Trp Leu  
 290 295 300  
 Pro Gly Ser Pro Ser Ala Glu Pro Gly Lys Ser Cys Val Ser Leu Asn  
 305 310 315 320  
 Pro Gly Lys Asn Ala Lys Trp Glu Asn Leu Glu Cys Val Gln Lys Leu  
 325 330 335  
 Gly Tyr Ile Cys Lys Lys Gly Asn Thr Thr Leu Asn Ser Phe Val Ile  
 340 345 350  
 Pro Ser Glu Ser Asp Val Pro Thr His Cys Pro Ser Gln Trp Trp Pro  
 355 360 365  
 Tyr Ala Gly His Cys Tyr Lys Ile His Arg Asp Glu Lys Lys Ile Gln  
 370 375 380  
 Arg Asp Ala Leu Thr Thr Cys Arg Lys Glu Gly Gly Asp Leu Thr Ser  
 385 390 395 400  
 Ile His Thr Ile Glu Glu Leu Asp Phe Ile Ile Ser Gln Leu Gly Tyr  
 405 410 415  
 Glu Pro Asn Asp Glu Leu Trp Ile Gly Leu Asn Asp Ile Lys Ile Gln  
 420 425 430  
 Met Tyr Phe Glu Trp Ser Asp Gly Thr Pro Val Thr Phe Thr Lys Trp  
 435 440 445

Leu Arg Gly Glu Pro Ser His Glu Asn Asn Arg Gln Glu Asp Cys Val  
 450 455 460  
 Val Met Lys Gly Lys Asp Gly Tyr Trp Ala Asp Arg Gly Cys Glu Trp  
 465 470 475 480  
 Pro Leu Gly Tyr Ile Cys Lys Met Lys Ser Arg Ser Gln Gly Pro Glu  
 485 490 495  
 Ile Val Glu Val Glu Lys Gly Cys Arg Lys Gly Trp Lys Lys His His  
 500 505 510  
 Phe Tyr Cys Tyr Met Ile Gly His Thr Leu Ser Thr Phe Ala Glu Ala  
 515 520 525  
 Asn Gln Thr Cys Asn Asn Glu Asn Ala Tyr Leu Thr Thr Ile Glu Asp  
 530 535 540  
 Arg Tyr Glu Gln Ala Phe Leu Thr Ser Phe Val Gly Leu Arg Pro Glu  
 545 550 555 560  
 Lys Tyr Phe Trp Thr Gly Leu Ser Asp Ile Gln Thr Lys Gly Thr Phe  
 565 570 575  
 Gln Trp Thr Ile Glu Glu Glu Val Arg Phe Thr His Trp Asn Ser Asp  
 580 585 590  
 Met Pro Gly Arg Lys Pro Gly Cys Val Ala Met Arg Thr Gly Ile Ala  
 595 600 605  
 Gly Gly Leu Trp Asp Val Leu Lys Cys Asp Glu Lys Ala Lys Phe Val  
 610 615 620  
 Cys Lys His Trp Ala Glu Gly Val Thr His Pro Pro Lys Pro Thr Thr  
 625 630 635 640  
 Thr Pro Glu Pro Lys Cys Pro Glu Asp Trp Gly Ala Ser Ser Arg Thr  
 645 650 655  
 Ser Leu Cys Phe Lys Leu Tyr Ala Lys Gly Lys His Glu Lys Lys Thr  
 660 665 670

Trp

SWIGGARD, WILLIAM J  
 JIANG, WANPING

- (ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Klauber & Jackson
  - (B) STREET: 411 Hackensack Avenue
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601

- (v) COMPUTER READABLE FORM:  
 (A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

- (vi) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: US 08/381,528  
 (B) FILING DATE: 31-JAN-1995  
 (C) CLASSIFICATION:

- (vii) CURRENT APPLICATION DATA:  
 (A) APPLICATION NUMBER: WO  
 (B) FILING DATE: 31-JAN-1996  
 (C) CLASSIFICATION:

- (viii) ATTORNEY/AGENT INFORMATION:  
 (A) NAME: Jackson Esq., David A.  
 (B) REGISTRATION NUMBER: 26,742  
 (C) REFERENCE/DOCKET NUMBER: 600-1-081

- (ix) TELECOMMUNICATION INFORMATION:  
 (A) TELEPHONE: 201 487-5800  
 (B) TELEFAX: 201 343-1684  
 (C) TELEX: 133521

(x) Note: In all the amino acid sequences below, "Xaa" stands for one of the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
 (A) DESCRIPTION: cytoplasmic domain of human DEC-205

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: C-terminal

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acid  
 SWIGGARD, WILLIAM J



JIANG, WANPING

(ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH  
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(iii) NUMBER OF SEQUENCES: 8

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(vii) CURRENT APPLICATION DATA:

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- (B) FILING DATE: 31-JAN-1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: cytoplasmic domain of human DEC-205

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:2:

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(A) LENGTH: 25 amino acid  
SWIGGARD, WILLIAM J  
JIANG, WANPING

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(vii) CURRENT APPLICATION DATA:  
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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
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- (iii) HYPOTHETICAL: NO
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1			5					10						15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20				25							30		

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  - SWIGGARD, WILLIAM J
  - JIANG, WANPING
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  - (C) CLASSIFICATION:
- (vii) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO

(B) FILING DATE: 31-JAN-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-081

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(B) TELEFAX: 201 343-1684  
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(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: peptide  
(A) DESCRIPTION: cytoplasmic domain of human DEC-205  
  
(iii) HYPOTHETICAL: NO  
  
(v) FRAGMENT TYPE: C-terminal  
  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: human  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1			5					10						15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:2:

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SWIGGARD, WILLIAM J  
JIANG, WANPING  
  
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(vii) CURRENT APPLICATION DATA:  
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(B) FILING DATE: 31-JAN-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
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(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-081

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(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(A) DESCRIPTION: cytoplasmic domain of human DEC-205

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
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SWIGGARD, WILLIAM J  
JIANG, WANPING

(ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH  
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(B) FILING DATE: 31-JAN-1995  
(C) CLASSIFICATION:

(vii) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: WO  
(B) FILING DATE: 31-JAN-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 600-1-081

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 201 487-5800  
(B) TELEFAX: 201 343-1684  
(C) TELEX: 133521

(x) Note: In all the amino acid sequences below, "Xaa" stands for one of  
the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(A) DESCRIPTION: cytoplasmic domain of human DEC-205

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1			5						10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20					25						30		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acid

SWIGGARD, WILLIAM J

JIANG, WANPING

(ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH  
C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND  
USES THEREOF

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Klauber & Jackson

(B) STREET: 411 Hackensack Avenue

(C) CITY: Hackensack

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/381,528

(B) FILING DATE: 31-JAN-1995

(C) CLASSIFICATION:

(vii) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: WO

(B) FILING DATE: 31-JAN-1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1			5					10						15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
		20					25						30		

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- (A) LENGTH: 25 amino acid
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- JIANG, WANPING

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- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: C-terminal
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	
Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp		
			20				25						30		

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        SWIGGARD, WILLIAM J  
        JIANG, WANPING
- (ii) TITLE OF INVENTION: IDENTIFICATION OF DEC, A RECEPTOR WITH C-TYPE LECTIN DOMAINS, NUCLEIC ACIDS ENCODING DEC, AND USES THEREOF
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(vii) CURRENT APPLICATION DATA:

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(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg His Arg Leu His Leu Ala Gly Phe Ser Ser Val Arg Tyr Ala Gln  
1                      5                      10                      15

Gly Val Asn Glu Asp Glu Ile Met Leu Pro Ser Phe His Asp  
20                      25                      30

(2) INFORMATION FOR SEQ ID NO:2:

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Arg	His	Arg	Leu	His	Leu	Ala	Gly	Phe	Ser	Ser	Val	Arg	Tyr	Ala	Gln
1				5					10					15	

Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp
			20				25					30	

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1			5					10						15	

Gly	Val	Asn	Glu	Asp	Glu	Ile	Met	Leu	Pro	Ser	Phe	His	Asp
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Gly Val Asn Glu Asp Glu Ile Met Leu Pro Ser Phe His Asp  
                    20                      25                      30

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